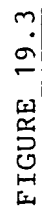
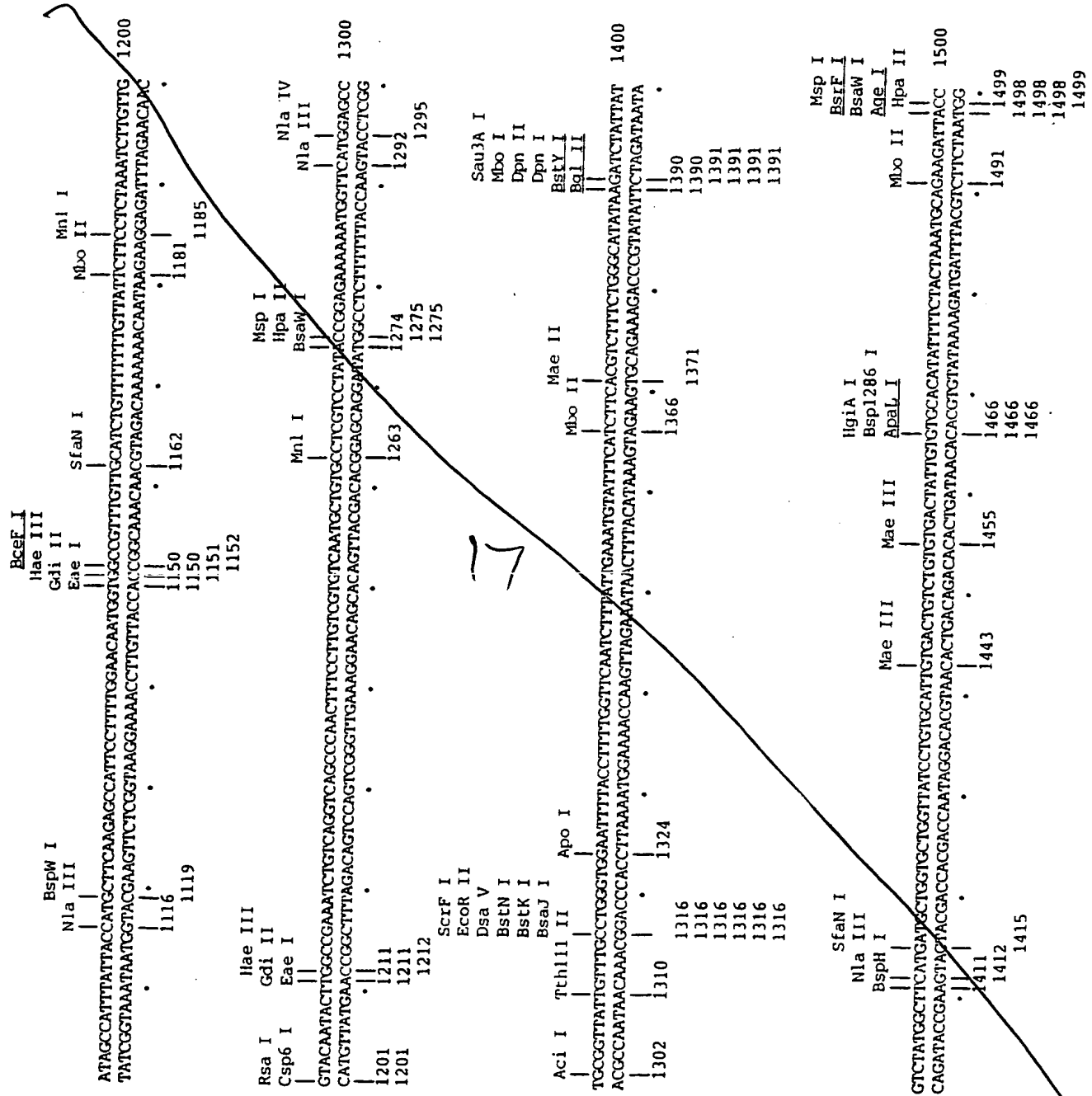


FIGURE 19.2



[illegible]

FIGURE 19.4

FIGURE 19.5

668060" 4226FE60

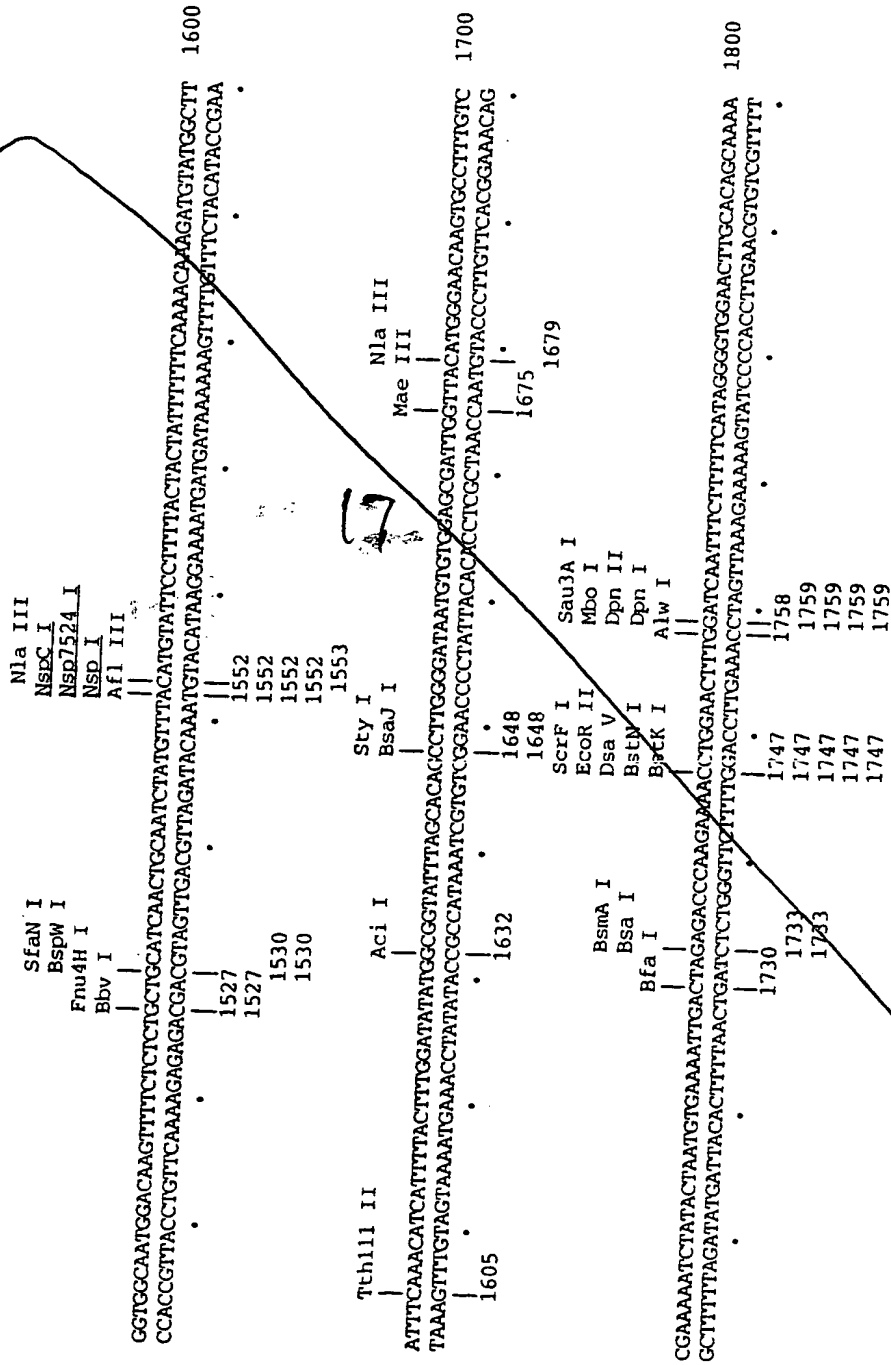


FIGURE 19.6

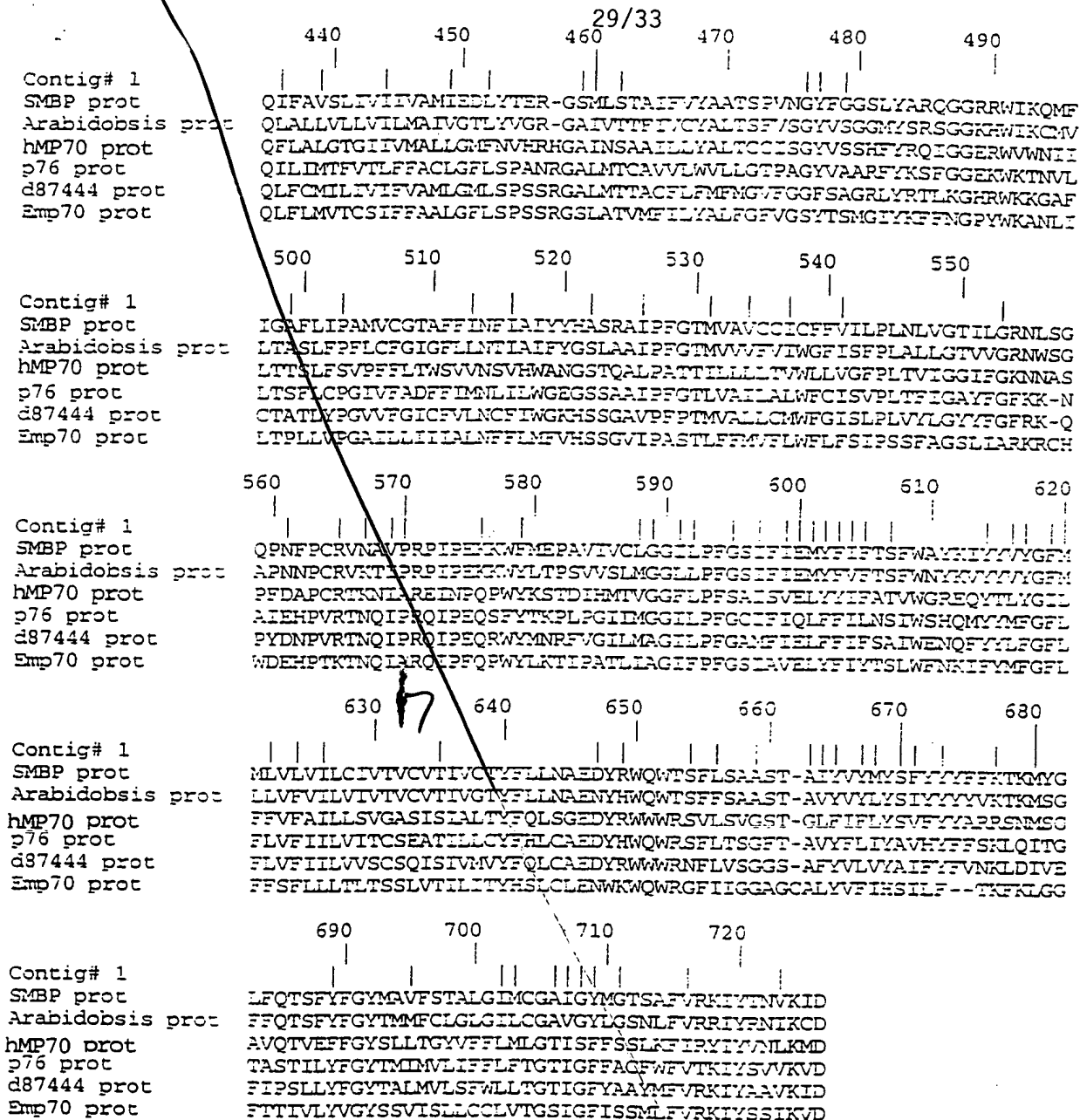


FIGURE 22.2

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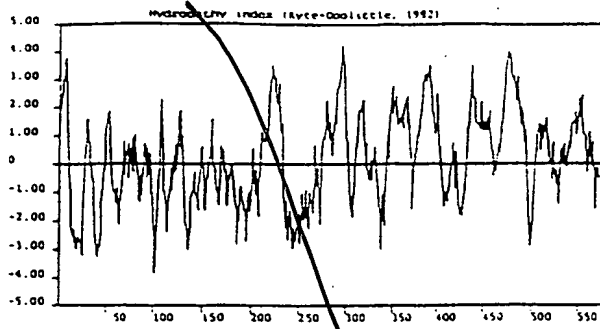
Contig# 1      |||
SMBP prot     SMILMRTLKDYARYSKEEE-MDD-MDRDLGD-EYGWKQVHGVDVFRPSSHPLIFSSLIGSGC
Arabidopsis prot SMILMRTLNDYAKYAREDDDLLES-LERDVSE-ESGWKLVEGVDVFRPASSLVLLSAVVGTTGA
hMP70 prot    AVILMRVLRLNDLARYNLDEETTSAGSGDDFDQGDNGWKI IHTDVFRFPVPRGLLCAVLGVGA
p76 prot     AMIMLRTLHKDLARYNQ-----MDSTED-AQEEFGWKLVEGVDIFRPPRKGMLLSVFLGSGT
d87444 prot  SMIIIRTLRKDLARYNK-----EDDIED-TMEESGWKLVEGVDVFRPPQPSYPMILSSLLGSGI
Emp70 prot    IHSLLRLKLSDFARYNE-----LNLDDD-FSDSGWKLNHGVDVFRSPQSYPMILSSLLGSGI

```

FIGURE 22.1

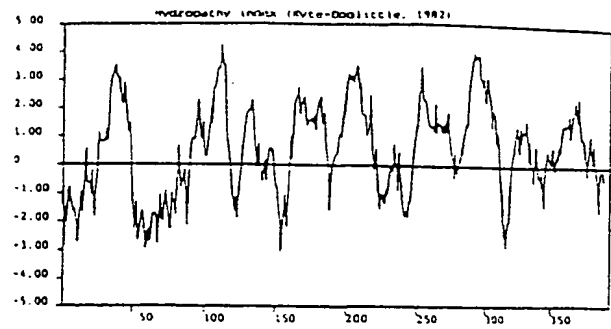
SMBP

A

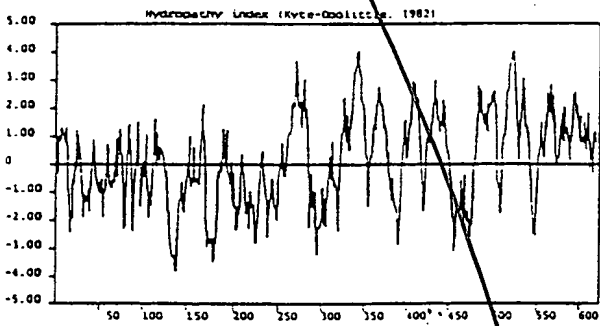


SMBP (C-ter)

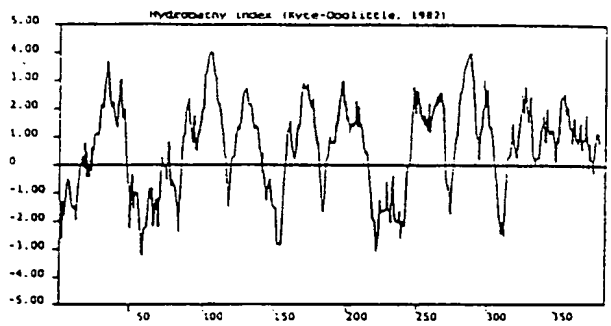
B



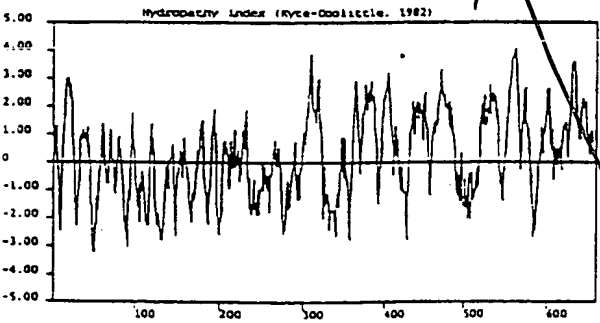
D87444



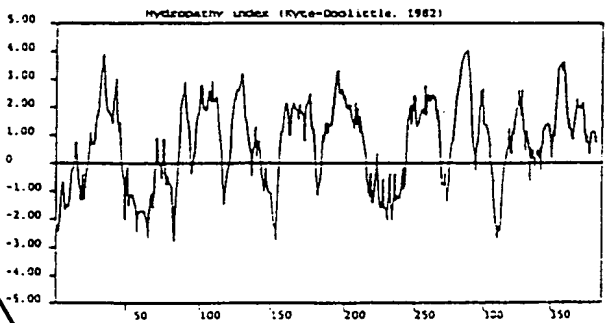
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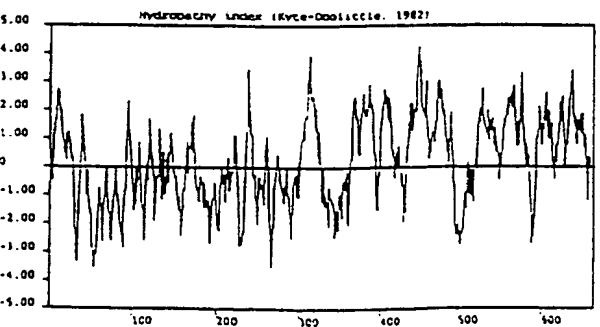
Hu p76



Hu p76 (C-ter)



Emp 70



Emp 70 (C-ter)

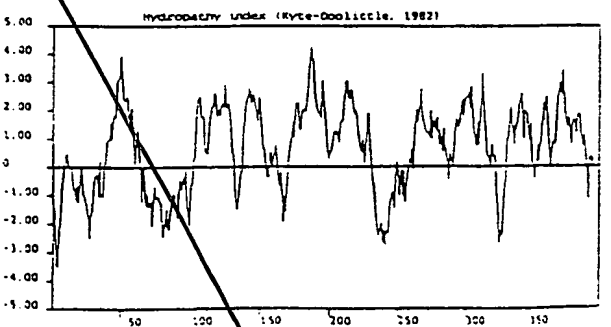


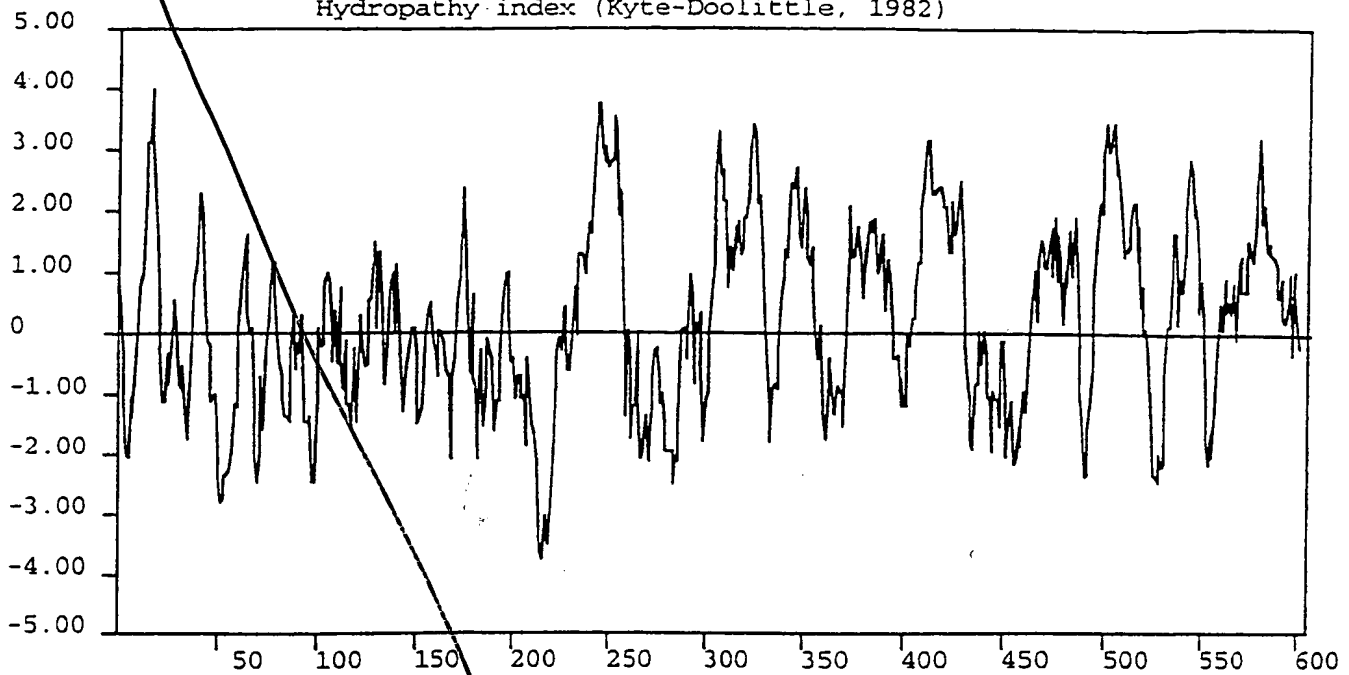
FIGURE 23.1

558060" 4246TE60

hMP70

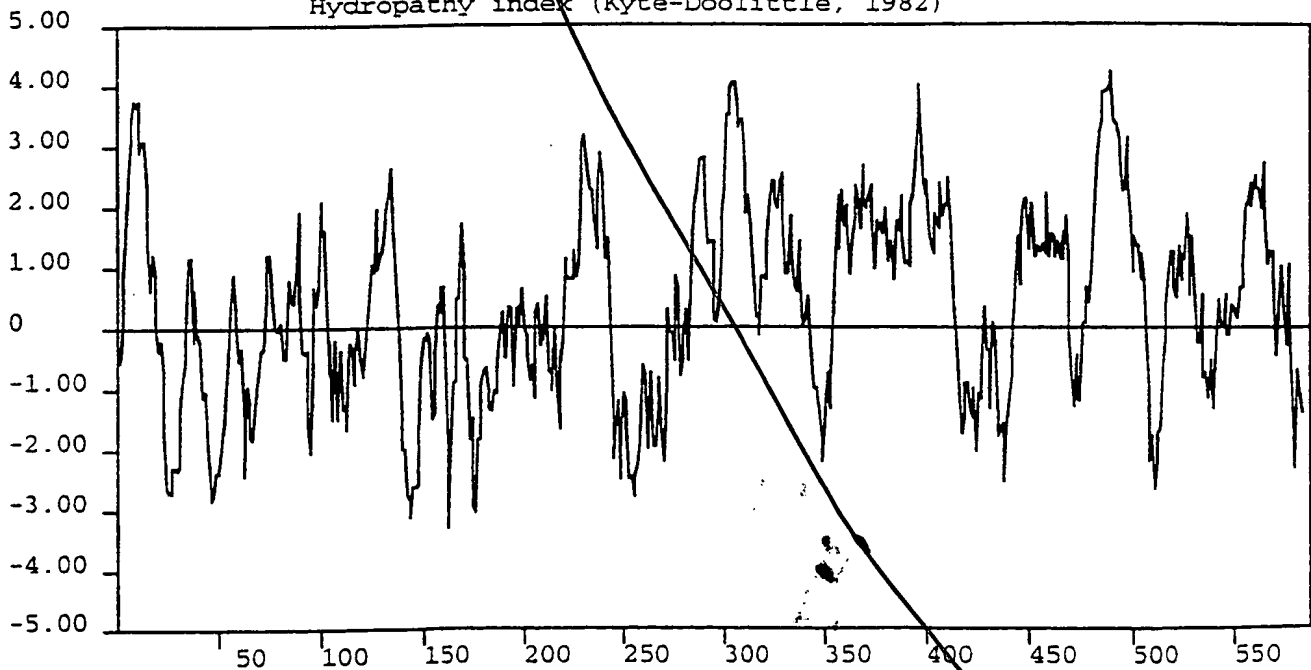
A

Hydropathy index (Kyte-Doolittle, 1982)



Arabidopsis
Hydropathy index (Kyte-Doolittle, 1982)

A

FIGURE 23.2

A)

1 CC GCC GCG CTG TGG CTG CTG CTG CTG CTG CCC CGG ACC CGG GCG GAC GAG CAC GAA CAC ACG TAT CAA GAT 74
1 A A L W L L L L L L L P R T R A D E H E H T Y Q D 24

75 AAA GAG GAA GTT GTT TTA TGG ATG AAT ACT GTT GCG CCC TAC CAT AAT CGT CAA GAA ACA TAT AAG TAC TTT TCA CTT CCA TTC TGT CTG 164
25 K E E V V L W H N T V G P Y H N R Q E T Y K Y P S L P F C V 54

165 GGG TCA AAA AAA AGT ATC AGT CAT TAC CAT GAA ACT CTG GGA GAA GCA CTT CAA GCG GTT GAA TTG GAA TTT AGT GGT CTG GAT ATT AAA 254
55 G S K K S I S H Y H E T L G E A L Q G V E L E F S G L D I K 84

255 TTT AAA GAT GAT GTG ATG CCA GCC ACT TAC TGT GAA ATT GAT TTA GAT AAA GAA AAG AGA GAT GCA TTT GTA TAT GCC ATA AAA AAT CAT 344
85 F K D D V M P A T Y C E I D L D K E K R D A F V Y A I K N H 114

345 TAC TGG TAC CAG ATG TAC ATA GAT GAT TTA CCA ATA TGG GGT ATT GTT GGT GAG GCT GAT GAA AAT GGA GAA GAT TAC TAT CTT TGG ACC 434
115 Y W Y Q M Y I D D L P I W G I V G E A D E N G E D Y Y L W T 144

435 TAT AAA AAA CTT GAA ATA GGT TTT AAT GGA AAT CGA ATT GTT GAT GTT AAT CTA ACT AGT GAA GGA AAG GTG AAA CTG GTT CCA AAT ACT 524
145 Y K K L E I G F Y G N R I V D V N L T S E G K V K L V P N T 174

525 AAA ATC CAG ATG TCA TAT TCA GTA AAA TGG AAA AAG TCA GAT GTG AAA TTT GAA GAT CGA TTT GAC AAA TAT CTT GAT CCG TCC TTT TTT 614
175 K I Q M S Y S V K W K K S D V K F E D R F D K Y L D P S F F 204

615 CAA CAT CGG ATT CAT TGG TTT TCA ATT TTT AAC TCC TTC ATG ATG GTG ATC TTC TTG GTG GCG TTA GTT TCA ATG ATT TTA ATG AGA ACA 704
205 Q B R I E W P S I P N S F M H V I F L V G L V S M I L H M R T 234

705 TTA AGA AAA GAT TAT GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG CAT AGA GAC CTA GGA GAT GAA TAT GGA TGG AAA CAG GTG 794
235 L R K D Y A R Y S K E E E M D G H D R D L G D E Y G W K Q V 264

795 CAT GGA GAT GTA TTT AGA CCA TCA AGT CAC CCA TGA ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG ATA TTT GCT VTG TCT CTC ATC 884
265 H G D V P R P S S H P I P S S L I G S G C Q I F A V S L I 294

885 GTT ATT ATT GTT GCA ATG ATA GAA GAT TTA TAT ACT GAG AGC GGA TCA ATG CTC AGT ACA GCC ATA TTT GTC TAT GCT GCT ACG TCT CCA 974
295 V I I V A M I E D L Y T R G S M L S T A I F V Y A A T S P 324

975 GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC CTT ATC CCA 1064
325 V N G Y P G G S L Y A R Q G G R R W I K Q M P I G A F L I P 354

1065 GCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA GCG ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG GCC 1154
355 A M V C G T A P F I N F I A I Y Y H A S R A I P F G T H V A 384

1155 GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CTT CTA AAT CTT GGT GGT ACA ATA CTT GGC CCA AAT CTG TCA GGT CAG CCC AAC TTT CCT 1244
385 V C C I C F F V I L P L N L V G T I L G R N L S G Q P N F P 414

1245 TGT GGT GTC AAT GCT GTG CCT GCT CCT ATA CCG GAG AAA AAA TGG TTC ATG GAG CCT GCG GTT ATT GTT TGC CTG CCG GCA ATT TTA GGT 1334
415 C R V N A V P R P I P E K K W F M E P A V I V C L G G I L P 444

1335 TTT GGT TCA ATG TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG CCA TAT AAG ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG 1424
445 F G S I F I E H Y F I P T S F W A Y K I Y Y V Y G F H M L V 474

1425 CTG GTT ATC CTG TGC ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA GAA GAT TAC CCG TGG CAA TGG ACA 1514
475 L V I L C I V T V C V T I V C T Y R L L N A E D Y R W Q W T 504

1515 AGT TTT CTC TCT GCT GCA TCA ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAT TAT TTT TTC AAA ACA AAG ATG TAT GGC TTA TTT 1604
505 S F L S A A S T A I Y V Y H Y S F Y Y Y F F K T K H Y G L F 534

1605 CAA ACA TCA TTT TAC TTT GGA TAT ATG GCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC ATG GGA ACA AGT GCC 1694
535 Q T S P Y P G Y H A V F S T A L G I N C G A I G Y H G T S A 564

1695 TTT GTC CGA AAA ATC TAT ACT AAT GTG AAA ATT GAC TAG AGACCAAGAAACCTGGAACCTTGGATCAATTCTTTTCATAGGGTGAACCTTGCACAGCAAAA 1800
565 P V R K I Y T N V K I D 576

B)

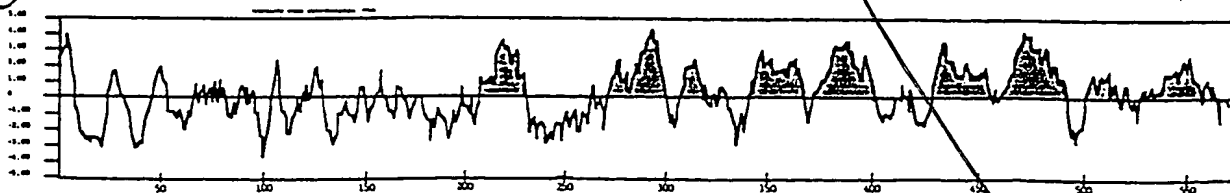


FIGURE 24